Attorney Docket No.:   **NE-0004**
Inventors: **Hollingsworth et al.**
Serial No.:   **10/618,481**
Filing Date: **July 11, 2003**
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Amendments to the Specification:

Please replace the paragraph beginning at page 28, line 16, with the following rewritten paragraph:

--Two web-based algorithms were used to analyze the amino acid sequence of MUC1 cytoplasmic tail for potential human and murine MHC class I and class II binding epitopes. The first algorithm, "SYFPEITHI," (Rammensee, et al (1999) *supra*) ~~was available at http://www.uni-tuebingen.de/uni/kxi/. This algorithm~~ ranks peptides according to a score taking into account the presence of primary and secondary MHC-binding anchor residues. The second algorithm, "BIMAS," (Parker, et al (1994) *supra*) ~~was available at http://bimas.dcrt.nih.gov/molbio/hla_bind/. This algorithm~~ ranks potential binding according to the predicted half-time of dissociation of peptide/MHC complexes.--